

Application No.: 047863817

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

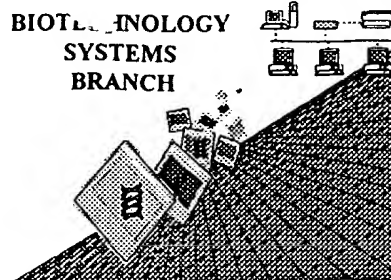
For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/863,818

Source: OIPF

Date Processed by STIC: 6-8-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/863, 818

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 ☒ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.
 SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.
 SEQ ID NO: 3 is primate DCRS6 reverse translation.
 SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.
 SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.
 SEQ ID NO: 6 is rodent DCRS6 reverse translation.
 SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.
 SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.
 SEQ ID NO: 9 is primate DCRS7 reverse translation.
 SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.
 SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.
 SEQ ID NO: 12 is rodent DCRS7 reverse translation.
 SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.
 SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.
 SEQ ID NO: 15 is primate DCRS8 reverse translation.
 SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.
 SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.
 SEQ ID NO: 18 is primate DCRS9 reverse translation.
 SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.
 SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.
 SEQ ID NO: 21 is rodent DCRS9 reverse translation.
 SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.
 SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.
 SEQ ID NO: 24 is primate DCRS10 reverse translation.
 SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.
 SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.
 SEQ ID NO: 27 is rodent DCRS10 reverse translation.
 SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.
 SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.
 SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.
 SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Gorman, Daniel M.

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01170K US

<140>

<141>

<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

<211> 1796

<212> DNA

<213> Unknown

<220>

Does Not Comply
Corrected Diskette Needed

pp. 1-7

Delete from
 beginning of file.
 Non-valid format.
 This information
 should be
 presented in the
 <220>, <223> feature
 field if the
 sequence is
 artificial or
 unknown, or in
 the <213> organism
 feature.

<223> Description of Unknown Organism: primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (4)..(1509)

<220>

<221> mat_peptide

<222> (46)..(1509)

<400> 1

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gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct	96
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser	
5 10 15	
cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp	
20 25 30	
ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca	192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser	
35 40 45	
att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc	240
Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg	
50 55 60 65	
ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag	288
Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln	
70 75 80	
tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag	336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln	
85 90 95	
acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct	384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro	
100 105 110	
gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat	432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
115 120 125	
gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca	480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser	
130 135 140 145	
cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag	528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys	
150 155 160	
gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag	576

Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu	
165 170 175	
gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac	624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr	
180 185 190	
atg gct ctt atc caa cac agc act atc atc ggg ttt tct cag gtg ttt	672
Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe	
195 200 205	
gag cca cac cag aag aaa caa acg cga gct tca gtg gtg att cca gtg	720
Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val	
210 215 220 225	
act ggg gat agt gaa ggt gct acg gtg cag ctg act cca tat ttt cct	768
Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro	
230 235 240	
act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc	816
Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys	
245 250 255	
cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa agc aag ccg	864
Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
260 265 270	
gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg	912
Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp	
275 280 285	
gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa agg atc aag	960
Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys	
290 295 300 305	
aag act tcc ttt tct acc acc aca cta ctg ccc ccc att aag gtt ctt	1008
Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu	
310 315 320	
gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att tgt tac ttc	1056
Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe	
325 330 335	
act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag	1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys	
340 345 350	
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Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala	
355 360 365	
act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac	1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp	
370 375 380 385	
gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	

390

395

400

agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc 1296
 Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys
 405 410 415

agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac 1344
 Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr
 420 425 430

ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc 1392
 Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
 435 440 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt 1440
 Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
 450 455 460 465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488
 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
 470 475 480

cac gat ggc tgc tgc tcc ttg tagccaccc atgagaagca agagacctta 1539
 His Asp Gly Cys Cys Ser Leu
 485

aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgacctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatata caataaaatt ttcaaattatt 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca 1779

ataaagcatc ttcagcc 1796

<210> 2

<211> 502

<212> PRT

<213> Unknown

Missing mandatory <220>, <223> features to
 explain the source of the unknown organism.
 See # 11 on the Error Summary Sheet.

<400> 2

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 -10 -5 -1 1

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 5 10 15

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 20 25 30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 35 40 45 50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 55 60 65

Note: This
 error occurs
 elsewhere in
 the sequence
 listing. Please
 review and
 correct.

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p.5

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 70 75 80
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
 85 90 95
 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
 100 105 110
 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
 115 120 125 130
 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
 135 140 145
 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
 150 155 160
 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
 165 170 175
 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
 180 185 190
 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
 195 200 205 210
 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
 215 220 225
 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
 230 235 240
 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
 245 250 255
 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
 260 265 270
 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
 275 280 285 290
 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
 295 300 305
 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
 310 315 320
 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
 325 330 335
 Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
 340 345 350
 Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
 355 360 365 370

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p 6

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
375 380 385

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
390 395 400

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
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Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
420 425 430

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
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Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
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His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
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Asp Gly Cys Cys Ser Leu
485

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p. 7

<210> 31
 <211> 178
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown Organism: worm; surmised
 Caenorabditis elegans

<400> 31

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Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val
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 35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
 50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
 65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
 85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
 100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
 115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
 130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
 145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
 165 170 175

Asn Ser

DX01170K US

1

→ Delete extraneous material
 from the end of the file. It
 causes format errors.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

F.Y.I. →